

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/203,548 1646DATE: 03/20/2000  
TIME: 12:44:09

INPUT SET: S35080.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information

(i) APPLICANT: Goli, Surya K.  
Hillman, Jennifer L.  
Murry, Lynn E.

(ii) TITLE OF THE INVENTION: NOVEL HUMAN CYTOKINE/STEROID  
RECEPTOR PROTEIN

(iii) NUMBER OF SEQUENCES: 4

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: US  
(F) ZIP: 94304

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 2.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/203,548  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/822,264  
(B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0233 US

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-845-4166  
(C) TELEX:

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# RAW SEQUENCE LISTING

## PATENT APPLICATION US/09/203,548

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### (2) INFORMATION FOR SEQ ID NO:1:

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#### (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 220 amino acids

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(B) TYPE: amino acid

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(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

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#### (vii) IMMEDIATE SOURCE:

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(A) LIBRARY: CONUTUT101

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(B) CLONE: 2504333

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#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
1      5      10      15
Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
20      25      30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
35      40      45
Asp Gln Pro Ala Ala Ser Gly Asp Arg Thr Thr Thr Xaa Pro Pro Pro
50      55      60
Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
65      70      75      80
Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
85      90      95
Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
100      105      110
Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
115      120      125
Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
130      135      140
Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe
145      150      155      160
Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu
165      170      175
Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ser Arg
180      185      190
Lys Asn Val Lys Ala Phe Ser Gly Ser Ile Ser Xaa Xaa Tyr Phe Ala
195      200      205
Lys Ser Phe Val Thr Val His Xaa Val Phe Lys Thr
210      215      220

```

### (2) INFORMATION FOR SEQ ID NO:2:

#### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 788 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

#### (vii) IMMEDIATE SOURCE:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/203,548

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(A) LIBRARY: CONUTUT101  
(B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

105	GCCGCCGAAC	CCCGCGCGCC	ACTCGCTCGC	TCAGAGGGAG	GAGAAAGTGG	CGAGTTCCGG	60
106	ATCCCTGCCCT	AGCGCGGCCC	AACCTTTTACT	CCAGAGATCA	TGGCTGCCGA	GGATGTGGTG	120
107	GCGACTGGCG	CCGACCCAAG	CGATCTGGAG	AGCGGCGGGC	TGCTGCATGA	GATTTTTCACG	180
108	TCGCCGCTCA	ACCTGCTGCT	GCTTGGCCTC	TGCATCTTCC	TGCTCTACAA	GATCGTGCGC	240
109	GGGGACCAGC	CGGCGGCCAG	CGGCGACAGG	ACGACGACGA	NGCCGCCCCC	TC TGCCCCCGC	300
110	CTCAAGCGGC	GCGACTTCAC	CCCCGCCGAG	CTGCGGCGCT	TCGACGGCGT	CCAGGACCCG	360
111	CGCATACTCA	TGGCCATCAA	CGGCAAGGTG	TTCGATGTGA	CCAAAGGCCG	CAAATTCTAC	420
112	GGGCCCCGAGG	GGCCGTATGG	GGTCTTTGCT	GGAAGAGATG	CATCCAGGGG	CCTTGCCACA	480
113	TTTTGCCTGG	ATAAGGAAGC	ACTGAAGGAT	GAGTACGATG	ACCTTTCTGA	CCTCACTGCT	540
114	GCCCAGCAGG	AGACTCTGAG	TGACTGGGAG	TCTCAGTTCA	CTTTCAAGTA	TCATCACGTG	600
115	GGCAAAGTGC	TGAAGGAGGG	GGAGGAGCCC	ACTGTGTACT	CAGATGAGGA	AGAACCAAAA	660
116	GATGAGAGTT	CCCGGAAAAA	TGTTAAAGCA	TTCAGTGGAA	GTATATCTAT	NNTGTATTTT	720
117	GCAAAATCAT	TTGTAACAGT	CCACTNTGTC	TTTAAACAT	AGTGTTACAA	TATTTAGAAA	780
118	GTTTGAGC						788

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank  
(B) CLONE: 158818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

134	Met	Ala	Ala	Glu	Asp	Val	Val	Ala	Thr	Gly	Ala	Asp	Pro	Ser	Glu	Leu
135	1			5					10						15	
136	Glu	Gly	Gly	Gly	Leu	Leu	Gln	Glu	Ile	Phe	Thr	Ser	Pro	Leu	Asn	Leu
137				20					25					30		
138	Leu	Leu	Leu	Gly	Leu	Cys	Ile	Phe	Leu	Leu	Tyr	Lys	Ile	Val	Arg	Gly
139				35				40					45			
140	Asp	Gln	Pro	Gly	Ala	Ser	Gly	Asp	Asn	Asp	Asp	Asp	Glu	Pro	Pro	Pro
141		50					55					60				
142	Leu	Pro	Arg	Leu	Lys	Pro	Arg	Asp	Phe	Thr	Pro	Ala	Glu	Leu	Arg	Arg
143		65				70				75					80	
144	Tyr	Asp	Gly	Val	Gln	Asp	Pro	Arg	Ile	Leu	Met	Ala	Ile	Asn	Gly	Lys
145				85					90					95		
146	Val	Phe	Asp	Val	Thr	Lys	Gly	Arg	Lys	Phe	Tyr	Gly	Pro	Glu	Gly	Pro
147				100					105					110		
148	Tyr	Gly	Val	Phe	Ala	Gly	Arg	Asp	Ala	Ser	Arg	Gly	Leu	Ala	Thr	Phe
149			115				120						125			
150	Cys	Leu	Asp	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Tyr	Asp	Asp	Leu	Ser	Asp
151		130					135					140				
152	Leu	Thr	Pro	Ala	Gln	Gln	Glu	Thr	Leu	Asn	Asp	Trp	Asp	Ser	Gln	Phe

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153      145      150      155      160
154      Ser Ser Pro Ser Ser Thr Ile Thr Trp Gly Lys Leu Leu Glu Gly Ala
155      165      170      175
156      Glu Glu Pro Ile Val Tyr Ser Asp Asp Glu Glu Gln Lys Met Arg Leu
157      180      185      190
158      Leu Gly Arg Val Thr Glu Ala Val Ser Gly Ala Tyr Leu Phe Leu Tyr
159      195      200      205
160      Phe Ala Lys Ser Phe Val Thr Phe Gln Ser Val Phe Thr Thr Trp
161      210      215      220
162

```

### (2) INFORMATION FOR SEQ ID NO:4:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

#### (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1657409

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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177      Met Ala Ala Glu Asp Val Ala Ala Thr Gly Ala Asp Pro Ser Glu Leu
178      1      5      10      15
179      Glu Gly Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
180      20      25      30
181      Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
182      35      40      45
183      Asp Gln Pro Ala Ala Ser Asp Ser Asp Asp Glu Pro Pro Pro Leu
184      50      55      60
185      Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg Phe
186      65      70      75      80
187      Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys Val
188      85      90      95
189      Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro Tyr
190      100      105      110
191      Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys
192      115      120      125
193      Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp Leu
194      130      135      140
195      Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe Thr
196      145      150      155      160
197      Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu Pro
198      165      170      175
199      Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg Lys
200      180      185      190
201      Asn Asp
202
203

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/203,548**

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